

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/069,290
Source:	PUTIO
Date Processed by STIC:	3/7/2002
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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
 - U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 1640 9, 290
attn: new rules cases	: Please disregard english "Alpha" headers, which were inserted by Pto Software
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8 Skipped Sequences (NEW RULES)	Sequence(s)missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
0Invalid <213> Response	Per 1.823 of Sequence Roles, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220><223> section is required when <213> response is Unknown or is Artificial Sequence.
1Use of <220>	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
2PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.
	A LOR OF Minushaulant Statema Branch - 08/21/2001



PCT10

RAW SEQUENCE LISTING DATE: 03/07/2002 PATENT APPLICATION: US/10/069,290 TIME: 15:24:35 Input Set : A:\pto.vsk.txt Output Set: N:\CRF3\03072002\J069290.raw Does N . Fompa orrection Fac Miles 2 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA 3 <120> TITLE OF INVENTION: Agent for enhancing expression of HM1.24 comprising as an active component interferon ? please use Western alphabetical 5 <130> FILE REFERENCE: H757 characters; otherwise, 6 <140> CURRENT APPLICATION NUMBER: US/10/069,290 6 <141> CURRENT FILING DATE: 2002-02-25 CRF program translates ERRORED SEQUENCES 8 <211> LENGTH: (1073) | 0|3 Shown $(\rho 2)$ 9 <212> TYPE: DNA ₩ 7 <210> SEQ ID NO: 1 > (2207 L- inset this mardatory 9 <212> TYPE: DNA 10 <213> ORGANISM: Homosapiens 11 <223> OTHER INFORMATION: Nucleotide sequence coding for HM1.24 protein antigen W- > 13 <400> SEQUENCE: 1 14 gaatteggea egagggatet gg atg gea tet aet teg tat gae tat tge Met Ala Ser Thr Ser Tyr Asp Tyr Cys 17 aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 18 Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Gly 15 20 145 20 ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 21 Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu 30 23 att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 24 Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu 50 26 cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 27 Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu 65 29 ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc 30 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala 32 acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 337 33 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu 95 100 35 aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 36 Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr

115

38 aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg

110

433



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002 TIME: 15:24:35

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

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	42	Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser '	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr	
	43			140					145					150				
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	51	tca	ccagt	itc t	tgago	gggt	c at	gggg	caac	acg	gtta	ıgcg	ggga	gago	ac g	ggggt	Lagccg	695
	52	gaga	aaggo	jcc t	tctgg	jagca	g gt	ctgg	gaggg	gcc	atgg	ggc	agto	ctgg	gt d	ctggg	ggacac	755
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	98	gtat	ccaa	ita a	ataa	cage	a ca	gcca	igaca	ttc	gggg	cca	ctac	cagt	.ct d	cgcg	gcattg	240
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	103	aca Baat	tacag agctg tcaat	gtaa gcaa tgct	tttt aatt aaga	aaag taga gagg	gg a ga g aa a	agag gaca ttca	acago caaco tcaat tttgo	g ga a aa t ct c cc	gaga cttt atta agag	ccca cggt ttat gtgc	ctg ttg cca acc	acco cagg catt	tgt gct tta tgg	gggg ggga cagc	getggte actgttt etgggga ecaatgt	360 420 480 540
	103 104	aca aat gca	tacag agctg tcaat aattc	gtaa gcaa tgct catg	tttt aatt aaga caat	aaag taga gagg tgtg	gg a ga g aa a at t	agag gaca ttca tccg	acago caaca tcaat tttgo accto	g ga a aa t ct c cc g gt	gaga cttt atta agag ccca	ccca cggt ttat gtgc aact	ctg ttg cca acc	acco cagg catt acco	tgt gct tta tgg aag	gggg ggga cagc cctc	getggte actgttt etgggga ecaatgt geaggee	360 420 480 540 600
	103 104 105	aca aat gca aga	tacag agctg tcaat aattc aacag	gtaa gcaa igct catg gtgc	tttt aatt aaga caat tgct	taaag taga igagg tgtg caaa	gg a ga g aa a at t ta a	agag gaca ttca tccg gtca	cacago rcaaca itcaat itttgo raccto	g ga a aa t ct c cc g gt a gt	gaga cttt atta agag ccca caaa	ccca cggt ttat gtgc aact	ttg cca acc acc tca	acco cagg catt acco ccta ggca	tgt gct tta tgg aag	gggg ggga cagc cctc ttag gtcg	getggte actgttt etgggga ecaatgt geaggee gtgtett	360 420 480 540 600 660
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	103 104 105 106 107 108 110 111	e acas aat gca aga aga at at acas at gga at gga	tacagagetg tcaattgaattgaacet tattca tgttt tgttt tggggt ggggt	gtaa gcaa ggct gtgc gga cagc attag cct cct	tttt aatt aaga caat tgct gtcc aaga ggtt ctcg agcc tctg	aaaga tagaga tagaga tagaga tagaga tagaga tagaga tagaga tagaga tagaga tagaa	gg agaataataagaataagaataagaataagaataagaataagaataa	agagggacactcagctcactgggacacacaggctgacacaggacacaggacacaggacacaggacacaggacacaggacagacaggacaggacagacagga	acaggacaataacaataacaacaacaacaacaacaacaacaacaa	gaat cogt gaat cogt gat cogt a cogt cogt a c	gaga cttt atta agag ccca cata tcta gggc gcct ctgt	ccca cggt ttat gtgc aact ttaag ctcg tcatg gggg	ctg ttg cca acc acc tca tgg tct cca gtg	accc cagg catt accc ccta ggca ggct atcc ggct ggtt tgct	tgt gct tta tgg aag agt tct ccc gaa	gggg gggg cagc cctc ttag gtcg tcac aagt aggg aagg	getggte actgttt etgggga ecaatgt geaggee gtgtett eceteag egattt ecgtgge etcagee ggettta ecettetg	360 420 480 540 600 660 720 780 840 900 960 1020 1080
	103 104 105 106 107 108 110 112 113	acas acas acas acas acas acas acas acas	tacagagetgeteattcattcattcattcattcattcattcattcattca	gtaa gcaa gct gtgc gtgc aggc attag cct cct ggaa	tttt aatt aaga caat tgct gtcc aaga ggtt ctcg agcc tctg	aaaga tagag tagag tagag tagag tagag tagag tagag tagag tagag tagaa	gg agaataagcaattaagctaacta	agagagagaca ttcagatca tccggctagacacacacacacacacacacacacacacaca	acago gcaaca ttcaat tttgo gctto gctto agctt atcco aacto gcato ttcgo gaato	gaat cogt gaat cogt gat cogt act act act act act act act act act ac	gaga cttta agaga ccaaa ccata tcta ggac ccat gccttg gctg	ccca cggt ttat gtgc aact actcac tcatg ccatg cctgg ctggt	ctg cca acc acc tca tcg cct gca gcc cca cca	acco catt acco ccta ggaca tggct atco ggtto tgct gatg	tgt gct ttgg aag act tcta ccc gaa	gggg gggg cagc cctc ttag gtcg tcac aagt agtgc aagt aaga ctga	getggte actgttt etgggga ecaatgt geaggee gtgtett eceteag etcagee etcagee ggettta ecttetg	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140
	103 104 105 106 107 108 110 111 113 114	acas acas acas acas acas acas acas acas	tacage to a get to a a cet to tet to a cet to te	gtaa gcaa ggct gtgc ggga catt atag ccct ctgg gaaa	tttt aatt aaga caat tgct gtcc aaga ggtt ctcg gctc tggc acat	aaaga tagagg tgtg caaa tggc tcatgc taaggg tgga tagac	gg agaataatcaagcaattaactaactaactaactaactaac	agagagagaca ttccg ttccg gtca gcta ttggg ttgg tt	cacago gcaaca itcaat itttgo gacto ggtago agctt gaccto gcato gcato gcato gcato gcato gcato gcato gcato gcato gcato	gaatcegateegateegateegg	gaga ctta agaca ccaaa ccaaa ccaaa tcta gccct gccgt gctgt tcat	ccca cggt ttat gtgc aact ttaac ttggt tcat gggg ctggt	ctg cca acc tca tcg tct gcct gcct gcct agc	accordance catta control catta control catta control catta c	tgt gttagg aaagt tctaa agt tctac ggg	gggg gggg cagc cctc ttag gtcg tcac aagt gtgc aagt aaga ctga	getggte actgttt etgggga ecaatgt geaggee gtgtett eceteag egatttt ecgtgge etcagee ggettta ecetetg aaaaaaa aagaage	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200
	103 104 105 106 107 108 110 111 113 114 115	acas acas acas acas acas acas acas acas	tacage to a get to a a cet to the a cet to the a cet to the a cet to the a cet go go cet go c	gtaa gcaa ggct gtgc gagc atag ccct gaaa gatt	tttt aatt aaga caat tgct gtcc aaga ggtt ctcg gctc tggc acat tcct	aaaga tagaga tagaga tagaga tagagaga tagaga tagaa	gg aga at a gcaact acctaactaactaactaactaactaactaactaa	agagagagaca ttccggctcac tccaggctcac ttggcacacagacacagacacagaccaca	cacago gcaaca ltcaat ltttgo gacto gctta ggtago aacto laacto gcato atcgco tcago tcago ltcago ltcago ltcago ltcago ltcago ltcago ltcago ltcaato	gaate gagtee gagtee to the total gagtee gagtee to gagtee to gagtee gagtee to the total	gaga ctta agca ccaa ccaa ccaa ccaa ccaa	ccca cggt ttat gtgc aact ttaac ttaggt ctggt tggc tggc	ctg cca acc acc tca tca tca gtg cct gcct agc cca cca cca agc cca	accordant can be accordant control can be accordant grant control can be accordant control can b	tgt gctagg aaagt tctacaa ggg agt	gggggggggggggggggggggggggggggggggggggg	getggte actgttt etgggga ecaatgt geaggee gtgtett eceteag egatttt ecgtgge etcagee ggettta ecateag aaaaaa agaagee egataat	360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260
	103 104 105 106 107 108 110 111 113 114 115	acas acas acas acas acas acas acas acas	tacage ago to a actor accept the accept to a accept to a accept to a accept acc	gtaa gcaa ggcg gtgc ggaact atag ccctgg gaaa gatt	ttttaattaaga caattget gtccaaga ggtt ctcg gctc tctg gctct tctg tct tcct ttcct ttcc	aaaga tagaga tagaga tagaga tagaga tagaga tagaga tagaa agaaga gaaga tagaaga tag	gg a ga a ta g c a c c c t c a c c c g t a c c a c c g t a c c a c c g t a c a c c c g t g t g t g t g t g t g t g t g	agagagagaca ttccg ttcca gctac ttggcac ttggcac acaggacac acaggacacac acagacacacac	cacago gcaaca ltcaat ltttgo gaccto ggttago cagctt gatco lactco la	gaatcottetcotagactotaa	gaga catta agcaa ccaa ccaaa ccaa ccaaa ccaaa ccaaa ccaa ccaaa ccaa ccaaa ccaa caa caa ccaa ccaa ccaa ccaa ccaa caa ccaa caa caa ccaa ccaa caa caa ccaa caa caa caa caa caa caa caa ca c	ccca cggt ttac (aact taac ttac ctggt ctatgg ctggt gcca ctgcca	ctg ttg cca acc tca tca tca gtg cca gag cag gag	accordant cattle acct a gac a	tgt gctagg aaagt tccaaggg tccaaggg agt	gggggggggggggggggggggggggggggggggggggg	getggte actgttt etgggga ecaatgt geaggee gtgtett eceteag egatttt ecgtgge etcagee ggettta ecetetg aaaaaaa aagaage	360 420 480 540 600 660 720 780 840 900 960 1020 1020 1140 1200 1260 1320





DATE: 03/07/2002 TIME: 15:24:35

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

PATENT APPLICATION: US/10/069,290

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118 agaccgacat tgtttgttgg ctgggtcggt ctcccagttt tcagctggct ccagtctcac 1440
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     120 atgaageest getegtease acagagacae etgaacacaa aaaccagtee etggggteag 1560
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     125 aagggetttt aaagcagggt gaaaaaaaa geecaeetee tttetgggaa aetgaaaetg 1860
     126 aaaacctaat taatcctctg cctgtaggtg cctcatgcaa gagctgctgg tcagagcact 1920
     127 teetggaact tgetattggt caggaegttt cetatgetaa taaaggggtg geeegtagaa 1980
     128 gattccagca coctecccta actccaggcc agactccttt cagctaaagg ggagatctgg 2040
     129 atg gca tct act tcg tat gac
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E-X 131
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WAL> 146 <220> FEATURE:
₩-/-> 147 <221> NAME/KEY:
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W7+> 310 <220> FEATURE:
312 <222> LOCATION:
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W--> 314 <400> SEQUENCE: 14
                                                                                       (37 )36
E--> 315 catggcatct acttcgtatg actattgcag agtgcc
     416 <210> SEQ ID NO: 25 (- last requere in file
     418 <212> TYPE: DNA
     419 <213> ORGANISM: Artificial Sequence
                                            sup4
₩(+)> 420 <220> FEATURE:
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002

TIME: 15:24:35

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

W/-> 421 <221> NAME/KEY:

422 <222> LOCATION:

423 <223> OTHER INFORMATION: Primer IRF2-R1

₩+→> 424 <400> SEQUENCE: 25

425 agtcggtacc ttaactgctc ttgacgcggg

30

E--> 426/1/12

E--> 428 - 1 - delete

selp 5 for more error

Please do not use bold print in the file Per 1.823 D. Seguera Kules, "A fixed-width font should be used exclusively throughout the Seguence Liters."

Do NOT change fonts

<210>	10
<211>	9
<212>	DNA
<213>	Artificial Sequence
<220>	1 10.4
<221>	6- all item 11 on Enor Summary Sheet
<222>	L- All wan 11 on
<223>	
<400>	10

For of real to the femore to the special to the spe



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002 TIME: 15:24:36

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier L:5 M:283 W: Missing Blank Line separator, <130> field identifier L:6 M:270 C: Current Application Number differs, Replaced Current Application No L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:6 M:283 W: Missing Blank Line separator, <160> field identifier L:7 M:283 W: Missing Blank Line separator, <210> field identifier L:13 M:283 W: Missing Blank Line separator, <400> field identifier L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1073 Found:1013 SEQ:1 L:63 M:283 W: Missing Blank Line separator, <400> field identifier L:94 M:283 W: Missing Blank Line separator, <400> field identifier L:131 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2016 Found:2061 SEQ:3 L:136 M:283 W: Missing Blank Line separator, <220> field identifier L:137 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4 L:140 M:283 W: Missing Blank Line separator, <400> field identifier L:146 M:283 W: Missing Blank Line separator, <220> field identifier L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5 L:150 M:283 W: Missing Blank Line separator, <400> field identifier L:151 M:252 E: No. of Seq. differs, <211> LENGTH:Input:78 Found:28 SEQ:5 L:157 M:283 W: Missing Blank Line separator, <400> field identifier L:199 M:283 W: Missing Blank Line separator, <400> field identifier L:248 M:283 W: Missing Blank Line separator, <220> field identifier L:249 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8 L:253 M:283 W: Missing Blank Line separator, <400> field identifier L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0 L:259 M:283 W: Missing Blank Line separator, <220> field identifier L:260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9 L:264 M:283 W: Missing Blank Line separator, <400> field identifier L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0L:270 M:283 W: Missing Blank Line separator, <220> field identifier L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10 L:274~M:283~W: Missing Blank Line separator, <400> field identifier L:280 M:283 W: Missing Blank Line separator, <220> field identifier L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11 L:284 M:283 W: Missing Blank Line separator, <400> field identifier L:290 M:283 W: Missing Blank Line separator, <220> field identifier L:291 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12 L:294 M:283 W: Missing Blank Line separator, <400> field identifier L:295 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:300 M:283 W: Missing Blank Line separator, <220> field identifier L:301 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13 L:304 M:283 W: Missing Blank Line separator, <400> field identifier L:310 M:283 W: Missing Blank Line separator, <220> field identifier L:311 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14 L:314 M:283 W: Missing Blank Line separator, <400> field identifier L:315 M:254 E: No. of Bases conflict, LENGTH:Input:37 Counted:36 SEQ:14 L:315 M:252 E: No. of Seq. differs, <211> LENGTH:Input:37 Found:36 SEQ:14 L:320 M:283 W: Missing Blank Line separator, <220> field identifier L:321 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002 TIME: 15:24:36

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

L:324 M:283 W: Missing Blank Line separator, <400> field identifier L:330 M:283 W: Missing Blank Line separator, <220> field identifier L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16 L:334 M:283 W: Missing Blank Line separator, <400> field identifier L:340 M:283 W: Missing Blank Line separator, <220> field identifier L:341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17 L:344 M:283 W: Missing Blank Line separator, <400> field identifier L:350 M:283 W: Missing Blank Line separator, <220> field identifier L:351 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18 $L:354\ M:283\ W:$ Missing Blank Line separator, <400> field identifier L:360 M:283 W: Missing Blank Line separator, <220> field identifier L:361 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19 L:364 M:283 W: Missing Blank Line separator, <400> field identifier L:370 M:283 W: Missing Blank Line separator, <220> field identifier L:371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20 L:374 M:283 W: Missing Blank Line separator, <400> field identifier L:380 M:283 W: Missing Blank Line separator, <220> field identifier L:381 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21 L:384 M:283 W: Missing Blank Line separator, <400> field identifier L:390 M:283 W: Missing Blank Line separator, <220> field identifier L:391 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22 L:394 M:283 W: Missing Blank Line separator, <400> field identifier L:400 M:283 W: Missing Blank Line separator, <220> field identifier L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23 L:404 M:283 W: Missing Blank Line separator, <400> field identifier L:410 M:283 W: Missing Blank Line separator, <220> field identifier L:411 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24 $L:414\ M:283\ W:$ Missing Blank Line separator, <400> field identifier L:420 M:283 W: Missing Blank Line separator, <220> field identifier L:421 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25 L:424 M:283 W: Missing Blank Line separator, <400> field identifier L:426 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:31 SEQ:25 L:426 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 M:254 Repeated in SeqNo=25 L:428 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:31 SEQ:25 L:6 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (25)